

1231-218.ST25.txt
SEQUENCE LISTING

<110> Mackenzie, Sally
Abdelnoor, Ricardo

<120> Implementation of a Mitochondrial Mutator

<130> 1231-218

<150> 60/456,318

<151> 2003-03-20

<160> 65

<170> PatentIn version 3.2

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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<223> n is a, c, g, or t

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<213> Hordeum vulgare

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<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

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Arg Asn Val Thr Ile Ser Leu Glu Gly Arg Pro Gln Pro Leu Tyr Leu
35          40          45

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Gly Thr Ala Thr Gln Ile Gly Val Ile Ser Thr Glu Gly Ile Pro Ser
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Leu Pro Lys Met Leu Leu Pro Pro Asn Cys Ala Gly Leu Pro Ser Met
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Tyr Ile Arg Asp Leu Leu Leu Asn Pro Pro Ser Phe Asp Val Ala Ser
Page 56

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Pro Glu Phe Thr Cys Ile Pro Ser Ala Lys Leu Val Lys Leu Leu Glu
 115 120 125

Ser Lys Glu Val Asn His Ile Glu Phe Cys Arg Ile Lys Asn Val Leu
 130 135 140

Asp Glu Ile Met Leu Met Asn Gly Ile Thr Glu Leu Ser Ala Ile Gln
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Asn Lys Leu Leu Glu Pro Ala Ser Val Val Thr Gly Leu Lys Val Asp
 165 170 175

Ala Asp Ile Leu Ile Lys Glu Cys Arg Phe Ile Ser Lys Arg Ile Gly
 180 185 190

Glu Val Ile Ser Leu Ala Gly Glu Ser Asp Gln Ala Ile Ser Ser Ser
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 35 40 45

Lys Arg Ser Ile Ser Glu Gln Ile Glu Val Val Cys Val Thr Val Gly
 50 55 60

Ala Arg Glu Gln Pro Pro Pro Ser Thr Val Gly Arg Ser Ser Ile Tyr
 65 70 75 80

Ile Ile Ile Arg Arg Asp Asn Lys Leu Tyr Val Gly Gln Thr Asp Asp
 85 90 95

Leu Val Gly Arg Leu Gly Ala His Arg Ser Lys Glu Gly Met Gln Asp
 100 105 110

Ala Thr Ile Leu Tyr Ile Val Val Pro Gly Lys Ser Val Ala Cys Gln
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Ser Gly Glu Ala Met Ala Ala His
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 <213> Hordeum vulgare

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caacagggttc ttttggactg ctgcgaaagg atgtcgagag cattgttact gcgatatgcg 120

aagacaagct gttggacctg tacaacaaga gaagcatctc agagcagatt gaggtggtct 180

1231-218.ST25.txt

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gtgtaactgt aggtgctagg gagcaaccgc caccttcaac cgttggcagg tccagcatct 240
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aaggttttta gctcaccaac aaggcagatg gcaagcatcg gaactttggt atgtctgtaa 480
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<210> 11
 <211> 444
 <212> DNA
 <213> Zea mays

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ctattgaata tccaatagca aaaagacctt cagctgacta gttccgctcga gtagcaactg 180
cctcgccaga gattcgagat ataccgaagt tcctgtgctt cccgtctgcc ttgttgatga 240
gcttgaagcc cctcgaaggg agctggttta tgagaagggg ttccagctgg caggcaacgc 300
tcttgccagg gaccaagacg tataataccg tagcgtcccc catgccttcc ttcgatctgt 360
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tgataatcac gtagatgcta gatc 444

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<210> 12
 <211> 94
 <212> PRT
 <213> Zea mays

<400> 12

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Ser Ser Ile Tyr Val Ile Ile Arg Ser Asp Asn Arg Leu Tyr Val Gly
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Gln Thr Asp Asp Leu Leu Gly Arg Leu Asn Ala His Arg Ser Lys Glu
          20           25           30

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Gly Met Arg Asp Ala Thr Val Leu Tyr Val Leu Val Pro Gly Lys Ser
          35           40           45

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Val Ala Cys Gln Leu Glu Thr Leu Leu Ile Asn Gln Leu Pro Ser Arg
          50           55           60

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Gly Phe Lys Leu Ile Asn Lys Ala Asp Gly Lys His Arg Asn Phe Gly
65           70           75           80

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1231-218.ST25.txt

Ile Ser Arg Ile Ser Gly Glu Ala Val Ala Thr Arg Arg Asn
85 90

<210> 13
<211> 338
<212> DNA
<213> *Medicago truncatula*

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cactgtaatc tgccaagatt ttatagcggg actgcgaagg aaaaagatca catcataact 180
tatcaagata aagtgtttct taattggcac tagggaatgg ccacctccga tgactatatg 240
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taatctcgag gatcgagttc gtgcacatcg atcgaaga 338

<210> 14
<211> 679
<212> DNA
<213> *Allium cepa*

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atgtttcttt tactgggcc 679

<210> 15
<211> 179
<212> PRT
<213> *Allium cepa*

<400> 15

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 Phe Ala Glu Val Asp Lys Ala Ala Gln Ser Leu Ser Ile Thr Val Met
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 Glu Asp Phe Val Pro Ile Val Ser Arg Val Lys Ala Val Met Ser Ser
 35 40 45
 Leu Gly Gly Pro Lys Gly Glu Val Cys Tyr Ala Arg Glu His Glu Ala
 50 55 60
 Val Trp Phe Lys Gly Lys Arg Phe Met Pro Ser Val Trp Ala Asn Thr
 65 70 75 80
 Pro Gly Glu Glu Gln Ile Lys Lys Leu Lys Pro Ala Leu Asp Ser Lys
 85 90 95
 Gly Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Ile Asn Ile Glu Asn
 100 105 110
 Ala Leu Thr Arg Tyr His Glu Ser Thr Glu Lys Ala Arg Ile Lys Val
 115 120 125
 Leu Asp Leu Leu Arg Glu Leu Ser Gly Glu Met Gln Ala Lys Ile Asn
 130 135 140
 Ile Leu Val Phe Ser Ser Met Leu Leu Val Ile Ser Lys Ser Leu Phe
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 His Asn Ser

<210> 16

<211> 662

<212> DNA

<213> Citrus sinensis

<400> 16

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 ttgatgctat catgcttcac atgaaatcct atgatagccc tgctgacggg aaaagctcat 240
 ttcagggtatt ctggttcctt gtactgaggt tgtaagtttg ctcatgccat gatagatcga 300

1231-218.ST25.txt

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 tt 662

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 <211> 81
 <212> PRT
 <213> Citrus sinensis
 <400> 17

Trp Phe Asp Ala Ala Glu Gly Ser Ala Val His Asn Thr Val Asp Met
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 20 25 30

Leu Leu Arg Ser Ile Cys Ala Ala Ser Leu Leu Gly Ile Cys Gly Leu
 35 40 45

Met Val Pro Ala Glu Ser Ala Ser Ile Pro Tyr Phe Asp Ala Ile Met
 50 55 60

Leu His Met Lys Ser Tyr Asp Ser Pro Ala Asp Gly Lys Ser Ser Phe
 65 70 75 80

Gln

<210> 18
 <211> 600
 <212> DNA
 <213> Solanum tuberosum

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attcgatgct tgtattcttg tggaatatgc tggtttaaatt ccatttggtg gcctgcgctc 540
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<210> 19
<211> 187
<212> PRT
<213> Solanum tuberosum

<400> 19

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20 25 30

Ser Phe Ser Pro His Thr Leu Cys Arg Glu Gln Ile Arg Cys Leu Lys
35 40 45

Glu Arg Lys Phe Phe Ala Thr Thr Ala Lys Lys Lys Leu Lys Gln Pro
50 55 60

Lys Ser Val Pro Glu Glu Lys Asp Tyr Val Asn Ile Met Trp Trp Lys
65 70 75 80

Glu Arg Met Glu Phe Leu Arg Lys Pro Ser Ser Val Leu Leu Ala Lys
85 90 95

Arg Leu Thr Tyr Cys Asn Leu Leu Gly Val Asp Pro Ser Leu Arg Asn
100 105 110

Gly Ser Leu Lys Glu Gly Thr Leu Asn Ser Glu Met Leu Leu Phe Lys
115 120 125

Ser Lys Phe Pro Arg Glu Val Leu Phe Cys Arg Val Gly Asp Phe Tyr
130 135 140

Glu Ala Ile Gly Phe Asp Ala Cys Ile Leu Val Glu Tyr Ala Gly Leu
145 150 155 160

Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro Lys Ala Gly Cys
165 170 175

Pro Val Val Asn Leu Arg Gln Thr Leu Asp Asp
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1231-218.ST25.txt

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 <211> 3396
 <212> DNA
 <213> Oryza sativa

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 <212> DNA

<213> Oryza sativa

<220>

<221> CDS

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<400> 21

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Arg	Trp	Leu	Pro	Val	Ala	Ala	Asp	Ser	Phe	Leu	Arg	Arg	Arg	His	Arg	
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cct	cgc	tgc	tcc	ccg	ctc	ccc	gcg	ctg	cta	ttt	aac	agg	agg	tcc	tgg	144
Pro	Arg	Cys	Ser	Pro	Leu	Pro	Ala	Leu	Leu	Phe	Asn	Arg	Arg	Ser	Trp	
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tct	aaa	cca	agg	aaa	gtc	tca	cga	agc	att	tcc	att	gtg	tct	agg	aag	192
Ser	Lys	Pro	Arg	Lys	Val	Ser	Arg	Ser	Ile	Ser	Ile	Val	Ser	Arg	Lys	
	50					55					60					

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Met	Asn	Lys	Gln	Gly	Asp	Leu	Cys	Asn	Glu	Gly	Met	Leu	Pro	His	Ile	
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ctg	tgg	tgg	aaa	gag	aaa	atg	gag	agg	tgc	agg	aaa	cca	tca	tca	atg	288
Leu	Trp	Trp	Lys	Glu	Lys	Met	Glu	Arg	Cys	Arg	Lys	Pro	Ser	Ser	Met	
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caa	ttg	act	cag	aga	ctt	gtg	tat	tca	aat	att	tta	gga	ttg	gat	cca	336
Gln	Leu	Thr	Gln	Arg	Leu	Val	Tyr	Ser	Asn	Ile	Leu	Gly	Leu	Asp	Pro	
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Leu	Gln	Phe	Lys	Ser	Lys	Phe	Pro	Arg	Glu	Val	Leu	Leu	Cys	Arg	Val	
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Gly	Asp	Phe	Tyr	Glu	Ala	Val	Gly	Phe	Asp	Ala	Cys	Ile	Leu	Val	Glu	
145				150						155					160	

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His	Ala	Gly	Leu	Asn	Pro	Phe	Gly	Gly	Leu	Arg	Ser	Asp	Ser	Ile	Pro	
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Lys	Ala	Gly	Cys	Pro	Val	Met	Asn	Leu	Arg	Gln	Thr	Leu	Asp	Asp	Leu	
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Thr	Arg	Cys	Gly	Tyr	Ser	Val	Cys	Ile	Val	Glu	Glu	Ile	Gln	Gly	Pro	
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acc	caa	gct	cgt	gct	agg	aaa	ggc	cga	ttt	att	tct	ggc	cat	gca	cat	672
Thr	Gln	Ala	Arg	Ala	Arg	Lys	Gly	Arg	Phe	Ile	Ser	Gly	His	Ala	His	
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1231-218.ST25.txt

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ggc Gly	tat Tyr	tgc Cys	ctg Leu 260	att Ile	tct Ser	gtg Val	cta Leu	gag Glu 265	aca Thr	atg Met	aaa Lys	aca Thr	tat Tyr 270	tca Ser	gct Ala	816
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cgt Arg	tat Tyr 290	cat His	cat His	cta Leu	tac Tyr	ctt Leu 295	cat His	agt Ser	tct Ser	ttg Leu	agg Arg 300	aac Asn	aat Asn	tct Ser	tca Ser	912
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gaa Glu	ctg Leu	tta Leu	tgc Cys 340	aag Lys	gta Val	agg Arg	gaa Glu	ata Ile 345	tat Tyr	ggg Gly	ctt Leu	gaa Glu 350	gag Glu	aag Lys	act Thr	1056
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ccc Pro 385	agt Ser	ttg Leu	cta Leu	aaa Lys	att Ile 390	gtt Val	ctc Leu	cct Pro	cca Pro	aac Asn 395	ttt Phe	ggt Gly	ggc Gly	ctt Leu	cca Pro 400	1200
tca Ser	ttg Leu	tat Tyr	att Ile	aga Arg 405	gat Asp	ctt Leu	ctt Leu	ctt Leu	aac Asn 410	cct Pro	cca Pro	tct Ser	ttt Phe	gat Asp 415	gtt Val	1248
gca Ala	tca Ser	tca Ser	gtt Val 420	caa Gln	gag Glu	gct Ala	tgc Cys	agg Arg 425	ctt Leu	atg Met	ggt Gly	agc Ser	ata Ile 430	act Thr	tgc Cys	1296
tcg Ser	att Ile	cct Pro 435	gaa Glu	ttt Phe	aca Thr	tgc Cys	ata Ile 440	ccg Pro	gca Ala	gca Ala	aag Lys	ctt Leu 445	gtg Val	aaa Lys	tta Leu	1344
ctc Leu	gag Glu 450	tca Ser	aaa Lys	gag Glu	gtt Val	aat Asn 455	cac His	atc Ile	gaa Glu	ttt Phe	tgt Cys 460	aga Arg	ata Ile	aag Lys	aat Asn	1392
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1231-218.ST25.txt

465		470		475		480										
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agt Ser 705	gaa Glu	gga Gly	cga Arg	aga Arg	agg Arg 710	ggg Gly	tgg Trp	gtg Val	ctt Leu	cct Pro 715	act Thr	ata Ile	tct Ser	ccc Pro	ttg Leu 720	2160
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1231-218.ST25.txt

Cys	Lys	Asp	Asn	Val 725	Thr	Glu	Glu	Ile	Ser 730	Ser	Glu	Met	Glu	Leu 735	Ser	
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aat Asn	gat Asp	gtc Val 755	cat His	atg Met	cac His	tct Ser	ttg Leu 760	ttt Phe	att Ile	ctt Leu	act Thr	ggt Gly 765	cca Pro	aac Asn	ggt Gly	2304
ggt Gly	ggt Gly 770	aaa Lys	tcc Ser	agt Ser	atg Met	ctg Leu 775	aga Arg	tca Ser	gtc Val	tgt Cys	gct Ala 780	gct Ala	gca Ala	tta Leu	ctt Leu	2352
gga Gly 785	ata Ile	tgt Cys	ggc Gly	ctg Leu	atg Met 790	gtg Val	cca Pro	gct Ala	gct Ala	tca Ser 795	gct Ala	gtc Val	atc Ile	cca Pro	cat His 800	2400
ttc Phe	gat Asp	tcc Ser	atc Ile	atg Met 805	ctg Leu	cat His	atg Met	aaa Lys	gca Ala 810	tat Tyr	gat Asp	agc Ser	cca Pro	gct Ala 815	gat Asp	2448
ggt Gly	aaa Lys	agt Ser	tcg Ser 820	ttt Phe	cag Gln	att Ile	gaa Glu	atg Met 825	tca Ser	gag Glu	ata Ile	cga Arg	tct Ser 830	tta Leu	gtc Val	2496
tgc Cys	cga Arg	gct Ala 835	aca Thr	gct Ala	agg Arg	agt Ser	ctt Leu 840	gtt Val	cta Leu	att Ile	gat Asp	gaa Glu 845	ata Ile	tgt Cys	agg Arg	2544
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gaa Glu	ggt Gly 930	atg Met	cct Pro	gac Asp	ttg Leu	ata Ile 935	att Ile	aga Arg	aga Arg	gct Ala	gag Glu 940	gaa Glu	cta Leu	tat Tyr	ttg Leu	2832
gct Ala 945	atg Met	agc Ser	aca Thr	aac Asn	agc Ser 950	aag Lys	cat His	aca Thr	tca Ser	tca Ser 955	gct Ala	gtc Val	cac His	cat His	gaa Glu 960	2880
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1231-218.ST25.txt

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 Tyr Leu Arg Asn Gly Leu Glu Leu Gln Ser Gly Ser Phe Gly Leu Leu
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aga aaa gaa att gag agt gtt gtt acc aca ata tgc aag aag aaa ctg 3024
 Arg Lys Glu Ile Glu Ser Val Val Thr Thr Ile Cys Lys Lys Lys Leu
 995 1000 1005

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 Leu Asp Leu Tyr Asn Lys Arg Ser Ile Ser Glu Leu Ile Glu Val
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ctc tat att gga cag acg gat gat ctt gtg ggt cga ctt agt gct 3204
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 His Arg Ser Lys Glu Gly Met Gln Asp Ala Thr Ile Leu Tyr Ile
 1070 1075 1080

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 Ile Asn Gln Leu Pro Leu Lys Gly Phe Lys Leu Ile Asn Lys Ala
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gat ggc aag cat cga aat ttc ggt ata tct ctt gtc cca gga gag 3384
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1231-218.ST25.txt

Ser Lys Pro Arg Lys Val Ser Arg Ser Ile Ser Ile Val Ser Arg Lys
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Met Asn Lys Gln Gly Asp Leu Cys Asn Glu Gly Met Leu Pro His Ile
65 70 75 80

Leu Trp Trp Lys Glu Lys Met Glu Arg Cys Arg Lys Pro Ser Ser Met
85 90 95

Gln Leu Thr Gln Arg Leu Val Tyr Ser Asn Ile Leu Gly Leu Asp Pro
100 105 110

Thr Leu Arg Asn Gly Ser Leu Lys Asp Gly Ser Leu Asn Thr Glu Met
115 120 125

Leu Gln Phe Lys Ser Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val
130 135 140

Gly Asp Phe Tyr Glu Ala Val Gly Phe Asp Ala Cys Ile Leu Val Glu
145 150 155 160

His Ala Gly Leu Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro
165 170 175

Lys Ala Gly Cys Pro Val Met Asn Leu Arg Gln Thr Leu Asp Asp Leu
180 185 190

Thr Arg Cys Gly Tyr Ser Val Cys Ile Val Glu Glu Ile Gln Gly Pro
195 200 205

Thr Gln Ala Arg Ala Arg Lys Gly Arg Phe Ile Ser Gly His Ala His
210 215 220

Pro Gly Ser Pro Tyr Val Phe Gly Leu Ala Glu Val Asp His Asp Val
225 230 235 240

Glu Phe Pro Asp Pro Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys
245 250 255

Gly Tyr Cys Leu Ile Ser Val Leu Glu Thr Met Lys Thr Tyr Ser Ala
260 265 270

Glu Glu Gly Leu Thr Glu Glu Ala Val Val Thr Lys Leu Arg Ile Cys
275 280 285

Arg Tyr His His Leu Tyr Leu His Ser Ser Leu Arg Asn Asn Ser Ser
290 295 300

1231-218.ST25.txt

Gly Thr Ser Arg Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly
305 310 315 320

Glu Cys Ser Gly Lys Ser Phe Glu Trp Phe Asp Gly Asn Pro Ile Glu
325 330 335

Glu Leu Leu Cys Lys Val Arg Glu Ile Tyr Gly Leu Glu Glu Lys Thr
340 345 350

Val Phe Arg Asn Val Ser Val Ser Leu Glu Gly Arg Pro Gln Pro Leu
355 360 365

Tyr Leu Gly Thr Ala Thr Gln Ile Gly Val Ile Pro Thr Glu Gly Ile
370 375 380

Pro Ser Leu Leu Lys Ile Val Leu Pro Pro Asn Phe Gly Gly Leu Pro
385 390 395 400

Ser Leu Tyr Ile Arg Asp Leu Leu Leu Asn Pro Pro Ser Phe Asp Val
405 410 415

Ala Ser Ser Val Gln Glu Ala Cys Arg Leu Met Gly Ser Ile Thr Cys
420 425 430

Ser Ile Pro Glu Phe Thr Cys Ile Pro Ala Ala Lys Leu Val Lys Leu
435 440 445

Leu Glu Ser Lys Glu Val Asn His Ile Glu Phe Cys Arg Ile Lys Asn
450 455 460

Val Leu Asp Glu Val Leu Phe Met Gly Ser Asn Ala Glu Leu Ser Ala
465 470 475 480

Ile Leu Asn Lys Leu Leu Asp Pro Ala Ala Ile Val Thr Gly Phe Lys
485 490 495

Val Glu Ala Asp Ile Leu Val Asn Glu Cys Ser Phe Ile Ser Gln Arg
500 505 510

Ile Ala Glu Val Ile Ser Leu Gly Gly Glu Ser Asp Gln Ala Ile Thr
515 520 525

Ser Ser Glu Tyr Ile Pro Lys Glu Phe Phe Asn Gly Met Glu Ser Ser
530 535 540

Trp Lys Gly Arg Val Lys Arg Val His Ala Glu Glu Glu Phe Ser Asn
Page 72

545 550 555 560
 Val Asp Ile Ala Ala Glu Ala Leu Ser Thr Ala Val Ile Glu Asp Phe
 565 570 575
 Leu Pro Ile Ile Ser Arg Val Lys Ser Val Met Ser Ser Asn Gly Ser
 580 585 590
 Ser Lys Gly Glu Ile Ser Tyr Ala Lys Glu His Glu Ser Val Trp Phe
 595 600 605
 Lys Gly Arg Arg Phe Thr Pro Asn Val Trp Ala Asn Thr Pro Gly Glu
 610 615 620
 Leu Gln Ile Lys Gln Leu Lys Pro Ala Ile Asp Ser Lys Gly Arg Lys
 625 630 635 640
 Val Gly Glu Glu Trp Phe Thr Thr Ile Lys Val Glu Asn Ala Leu Thr
 645 650 655
 Arg Tyr His Glu Ala Cys Asp Asn Ala Lys Arg Lys Val Leu Glu Leu
 660 665 670
 Leu Arg Gly Leu Ser Ser Glu Leu Gln Asp Lys Ile Asn Val Leu Val
 675 680 685
 Phe Cys Ser Thr Met Leu Ile Ile Thr Lys Ala Leu Phe Gly His Val
 690 695 700
 Ser Glu Gly Arg Arg Arg Gly Trp Val Leu Pro Thr Ile Ser Pro Leu
 705 710 715 720
 Cys Lys Asp Asn Val Thr Glu Glu Ile Ser Ser Glu Met Glu Leu Ser
 725 730 735
 Gly Thr Phe Pro Tyr Trp Leu Asp Thr Asn Gln Gly Asn Ala Ile Leu
 740 745 750
 Asn Asp Val His Met His Ser Leu Phe Ile Leu Thr Gly Pro Asn Gly
 755 760 765
 Gly Gly Lys Ser Ser Met Leu Arg Ser Val Cys Ala Ala Ala Leu Leu
 770 775 780
 Gly Ile Cys Gly Leu Met Val Pro Ala Ala Ser Ala Val Ile Pro His
 785 790 795 800

1231-218.ST25.txt

Phe Asp Ser Ile Met Leu His Met Lys Ala Tyr Asp Ser Pro Ala Asp
805 810 815

Gly Lys Ser Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Val
820 825 830

Cys Arg Ala Thr Ala Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg
835 840 845

Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Ile Ile Glu
850 855 860

Arg Leu Asp Asn Val Gly Cys Ile Gly Ile Ile Ser Thr His Leu His
865 870 875 880

Gly Ile Phe Asp Leu Pro Leu Ser Leu His Asn Thr Asp Phe Lys Ala
885 890 895

Met Gly Thr Glu Ile Ile Asp Arg Cys Ile Gln Pro Thr Trp Lys Leu
900 905 910

Met Asp Gly Ile Cys Arg Glu Ser Leu Ala Phe Gln Thr Ala Arg Lys
915 920 925

Glu Gly Met Pro Asp Leu Ile Ile Arg Arg Ala Glu Glu Leu Tyr Leu
930 935 940

Ala Met Ser Thr Asn Ser Lys His Thr Ser Ser Ala Val His His Glu
945 950 955 960

Ile Ser Ile Ala Asn Ser Thr Val Asn Ser Leu Val Glu Lys Pro Asn
965 970 975

Tyr Leu Arg Asn Gly Leu Glu Leu Gln Ser Gly Ser Phe Gly Leu Leu
980 985 990

Arg Lys Glu Ile Glu Ser Val Val Thr Thr Ile Cys Lys Lys Lys Leu
995 1000 1005

Leu Asp Leu Tyr Asn Lys Arg Ser Ile Ser Glu Leu Ile Glu Val
1010 1015 1020

Val Cys Val Ala Val Gly Ala Arg Glu Gln Pro Pro Pro Ser Thr
1025 1030 1035

Val Gly Arg Ser Ser Ile Tyr Val Ile Ile Arg Arg Asp Ser Lys
1040 1045 1050

1231-218.ST25.txt

Leu Tyr Ile Gly Gln Thr Asp Asp Leu Val Gly Arg Leu Ser Ala
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His Arg Ser Lys Glu Gly Met Gln Asp Ala Thr Ile Leu Tyr Ile
1070 1075 1080

Leu Val Pro Gly Lys Ser Ile Ala Cys Gln Leu Glu Thr Leu Leu
1085 1090 1095

Ile Asn Gln Leu Pro Leu Lys Gly Phe Lys Leu Ile Asn Lys Ala
1100 1105 1110

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1115 1120 1125

Ala Ile Ala Ala
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caccatatgc cgccccaatt ttgtgagatg aattatcagt ggtgctaccc ttgtgcatag 360
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aatgcaatga cac 433

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1231-218.ST25.txt

Ser Arg Gly Phe Lys Leu Ile Asn Lys Ala Asp Gly Lys His Arg Asn
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Asp Ser Ile Met Leu His Met Lys Ala Tyr Asp Ser Pro Ala Asp Gly
35 40 45

Lys Ser Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ala Leu Val Ser
50 55 60

Arg Ala Thr Ala Arg Ser Leu Val Leu Ile Gly Glu Ile Cys Arg Gly
Page 76

65

70

75

80

Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Ile Ile Glu Arg
 85 90 95

Leu Asp Asn Val Gly Cys Leu Gly Ile Ile Ser Thr His Leu His Gly
 100 105 110

Ile Phe Asp Leu Pro Leu Ser Leu Ser Thr Thr Asp Phe Lys Ala Met
 115 120 125

Gly Thr Glu Val Val Asp Gly Cys Ile His Pro Thr Trp Lys Leu Met
 130 135 140

Asp Gly Ile Cys Arg Glu Ser Leu Ala Phe Gln Thr Ala Arg Arg Glu
 145 150 155 160

Gly Met Pro Glu Phe Ile Ile Arg Arg Ala Glu Glu Leu Tyr Leu Thr
 165 170 175

Met Ser Thr Asn Asn Lys Gln Thr Ala Ser Met Val His Asn Glu Pro
 180 185 190

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 195 200 205

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 gtcaagcaat cticagaaga atatgtcttc atgggtctcta gtaccatatt aatgcaataa 300
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1231-218.ST25.txt

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 gcagtcactg aagattttgt tcctgtagtt gctagaataa aggctattgt agcccctctc 360
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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt

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Lys Lys Pro Lys Ile Pro Asn Asn Val Leu Asp Asp Lys Asp Leu Pro
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 85 90 95

Thr Val Gln Leu Ile Glu Arg Leu Glu Phe Ser Asn Leu Leu Gly Leu
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Asn Ser Asn Leu Lys Asn Gly Ser Leu Lys Glu Gly Thr Leu Asn Trp
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Glu Met Leu Gln Phe Lys Ser Lys Phe Pro Arg Gln Val Leu Leu Cys
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Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Ile Leu
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1231-218.ST25.txt

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275 280 285

Thr Cys Gln Tyr His Tyr Leu Phe Leu His Thr Ser Leu Arg Arg Asn
290 295 300

Ser Cys Gly Thr Cys Asn Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu
305 310 315 320

Trp Gly Glu Cys Ser Ser Arg His Phe Asp Trp Phe Asp Gly Asn Pro
325 330 335

Val Ser Asp Leu Leu Ala Lys Val Lys Glu Leu Tyr Ser Ile Asp Asp
340 345 350

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Pro Leu Thr Leu Gly Thr Ser Thr Gln Ile Gly Ala Ile Pro Thr Glu
370 375 380

Gly Ile Pro Ser Leu Leu Lys Val Leu Leu Pro Ser Asn Cys Asn Gly
385 390 395 400

Leu Pro Val Leu Tyr Ile Arg Glu Leu Leu Leu Asn Pro Pro Ser Tyr
405 410 415

Glu Ile Ala Ser Lys Ile Gln Ala Thr Cys Lys Leu Met Ser Ser Val
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435 440 445

Lys Leu Leu Glu Trp Arg Glu Val Asn His Met Glu Phe Cys Arg Ile
450 455 460

Lys Asn Val Leu Asp Glu Ile Leu Gln Met Tyr Ser Thr Ser Glu Leu
Page 86

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 485 490 495
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 Ile Asn Ser Phe Ser Phe Ile Pro His Glu Phe Phe Glu Asp Met Glu
 530 535 540
 Ser Lys Trp Lys Gly Arg Ile Lys Arg Ile His Ile Asp Asp Val Phe
 545 550 555 560
 Thr Ala Val Glu Lys Ala Ala Glu Ala Leu His Ile Ala Val Thr Glu
 565 570 575
 Asp Phe Val Pro Val Val Ser Arg Ile Lys Ala Ile Val Ala Pro Leu
 580 585 590
 Gly Gly Pro Lys Gly Glu Ile Ser Tyr Ala Arg Glu Gln Glu Ala Val
 595 600 605
 Trp Phe Lys Gly Lys Arg Phe Thr Pro Asn Leu Trp Ala Gly Ser Pro
 610 615 620
 Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys Gly
 625 630 635 640
 Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ala Ala
 645 650 655
 Leu Thr Arg Tyr His Glu Ala Asn Ala Lys Ala Lys Glu Arg Val Leu
 660 665 670
 Glu Ile Leu Arg Gly Leu Ala Ala Glu Leu Gln Tyr Ser Ile Asn Ile
 675 680 685
 Leu Val Phe Ser Ser Met Leu Leu Val Ile Ala Lys Ala Leu Phe Ala
 690 695 700
 His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu Val
 705 710 715 720

1231-218.ST25.txt

Glu Ser His Gly Phe Glu Asp Val Lys Ser Leu Asp Lys Thr His Gly
 725 730 735
 Met Lys Ile Ser Gly Leu Leu Pro Tyr Trp Phe His Ile Ala Glu Gly
 740 745 750
 Val Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr Gly
 755 760 765
 Pro Asn Gly Gly Gly Lys Ser Ser Phe Leu Arg Ser Ile Cys Ala Ala
 770 775 780
 Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala Leu
 785 790 795 800
 Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp Ser
 805 810 815
 Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu Arg
 820 825 830
 Ser Ile Ile Gly Gly Thr Thr Asn Arg Ser Leu Val Leu Val Asp Glu
 835 840 845
 Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser
 850 855 860
 Ile Ile Glu Thr Leu Asp Gly Ile Gly Cys Leu Gly Ile Val Ser Thr
 865 870 875 880
 His Leu His Gly Ile Phe Thr Leu Pro Leu Asn Lys Lys Asn Thr Val
 885 890 895
 His Lys Ala Met Gly Thr Thr Ser Ile Asp Gly Gln Ile Met Pro Thr
 900 905 910
 Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu Thr
 915 920 925
 Ala Lys Arg Glu Gly Ile Pro Glu His Ile Val Arg Arg Ala Glu Tyr
 930 935 940
 Leu Tyr Gln Leu Val Tyr Ala Lys Glu Met Leu Phe Ala Glu Asn Phe
 945 950 955 960
 Pro Asn Glu Glu Lys Phe Ser Thr Cys Ile Asn Val Asn Asn Leu Asn
 965 970 975

1231-218.ST25.txt

Gly Thr His Leu His Ser Lys Arg Phe Leu Ser Gly Ala Asn Gln Met
980 985 990

Glu Val Leu Arg Glu Glu Val Glu Arg Ala Val Thr Val Ile Cys Gln
995 1000 1005

Asp His Ile Lys Asp Leu Lys Cys Lys Lys Ile Ala Leu Glu Leu
1010 1015 1020

Thr Glu Ile Lys Cys Leu Ile Ile Gly Thr Arg Glu Leu Pro Pro
1025 1030 1035

Pro Ser Val Val Gly Ser Ser Ser Val Tyr Val Met Phe Arg Pro
1040 1045 1050

Asp Lys Lys Leu Tyr Val Gly Glu Thr Asp Asp Leu Glu Gly Arg
1055 1060 1065

Val Arg Arg His Arg Leu Lys Glu Gly Met His Asp Ala Ser Phe
1070 1075 1080

Leu Tyr Phe Leu Val Pro Gly Lys Ser Leu Ala Cys Gln Phe Glu
1085 1090 1095

Ser Leu Leu Ile Asn Gln Leu Ser Gly Gln Gly Phe Gln Leu Ser
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Asn Ile Ala Asp Gly Lys His Arg Asn Phe Gly Thr Ser Asn Leu
1115 1120 1125

Tyr Thr
1130

<210> 32
<211> 757
<212> DNA
<213> Saccharum officinarum

<220>
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<222> (512)..(512)
<223> n is a, c, g, or t

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ggacgcgacg ccggcgcgga gacgcggcgt ctcgaagcac tagccccctg ttgttcttcc 120
gcgccggcgc gccggcgcca tgcaccgggt gctcgtgagc tcgctcgtgg ccgccacgcc 180

1231-218.ST25.txt

gcggtggctc cccctcgccg actccatcct ccggcgccgc cgcccgcgct gctcccctct 240
 tcccatgctg ctattcgacc ggaggacttg gtccaagcca aggaaggctc cacgaggcat 300
 ttcagtggca tctaggaaag ctaacaaaca gggagaatat tgtgatgaaa gcatgctatc 360
 tcatatcatg tgggtggaaag agaaaatgga gaagtgcaga aaaccatcat ctgtacagtt 420
 gactcagagg cttgtgtatt cgaatatatt agggttggat ccgaatttaa gaaatggaag 480
 cttgaaagat ggaaccctga acatggagat tntgctatit aaatcaaaaat ttcctcgtga 540
 ggttctactt tgcagaaaca tgcaggctta aattctcttt ggaggggttg gttctgacag 600
 aattcctaaa gctgggtgtc cagccggaat ttacggagac attggatgag ttgactcgat 660
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 gtcgattaat tctgggcatg cccatcctgg agcccta 757

<210> 33
 <211> 139
 <212> PRT
 <213> Saccharum officinarum

<220>
 <221> misc_feature
 <222> (125)..(125)
 <223> Xaa can be any naturally occurring amino acid

<400> 33

Met His Arg Val Leu Val Ser Ser Leu Val Ala Ala Thr Pro Arg Trp
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Leu Pro Leu Ala Asp Ser Ile Leu Arg Arg Arg Arg Pro Arg Cys Ser
 20 25 30

Pro Leu Pro Met Leu Leu Phe Asp Arg Arg Thr Trp Ser Lys Pro Arg
 35 40 45

Lys Val Ser Arg Gly Ile Ser Val Ala Ser Arg Lys Ala Asn Lys Gln
 50 55 60

Gly Glu Tyr Cys Asp Glu Ser Met Leu Ser His Ile Met Trp Trp Lys
 65 70 75 80

Glu Lys Met Glu Lys Cys Arg Lys Pro Ser Ser Val Gln Leu Thr Gln
 85 90 95

Arg Leu Val Tyr Ser Asn Ile Leu Gly Leu Asp Pro Asn Leu Arg Asn
 100 105 110

Gly Ser Leu Lys Asp Gly Thr Leu Asn Met Glu Ile Xaa Leu Phe Lys
 Page 90

115 120 1231-218.ST25.txt 125

Ser Lys Phe Pro Arg Glu Val Leu Leu Cys Arg
130 135

<210> 34
<211> 504
<212> DNA
<213> Saccharum officinarum

<400> 34
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tgctaccacc ctatacatct tggttcctgg caagagcgtt gcctgccagc tagaaaccct 180
tctcataaat cagcttcctt ctgagggcct caagctcatc aacaaggtag acggaaagca 240
taggaacttc ggtatatttc gaatctctgg agaggcaatt gctactcaac taaactaatc 300
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aggcaggagc taactgacac catgccgccc caatattggt gaactgatag cggagctagc 420
cttgaccata atacgggcat ctttttctcg tctaattgat tagtacaatg caaatgatta 480
gcaatgcaat gacactcgtt gtgc 504

<210> 35
<211> 72
<212> PRT
<213> Saccharum officinarum

<400> 35

Gly Arg Leu His Ala His Arg Gly Glu Glu Gly Met Gln Asp Ala Thr
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20 25 30

Thr Leu Leu Ile Asn Gln Leu Pro Ser Glu Gly Phe Lys Leu Ile Asn
35 40 45

Lys Val Asp Gly Lys His Arg Asn Phe Gly Ile Phe Arg Ile Ser Gly
50 55 60

Glu Ala Ile Ala Thr Gln Leu Asn
65 70

<210> 36
<211> 671
<212> DNA
<213> Nicotiana tabacum

1231-218.ST25.txt

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<400> 36
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aataaagaat gtggtcgatg aaatactgca gatgtacaga aattcagagc ttcgtgctat 180
tttagagtca gctgatggat cctacttggg tggcaaccgg gttaaaagtc gattttgata 240
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gtgaaagtga tcaaaagata agtccctatc ctatcatccc aaatgatttt tttgaagata 360
tggagtcgcc atggaaagggt cgtgtcaaga ggatccattt ggaggaagca tatgcagaag 420
tagacaaggc tgcagatgct ttatctttgg ctgtgagtct ctttttattt atcttcaaca 480
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aaataaaca g 671

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<210> 37
<211> 488
<212> DNA
<213> Lycopersicon esculentum

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<400> 37
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cattccattc agaaatgtca ctgttgtttc agaaaatagg ccccgctcct tacaccttgg 180
aactgccaca caaattggtg ctattccaac cgaagggatt ccatgtttgt taaagggtgtt 240
gcttcctcct cattgcagtg gtctaccagt cctgtatatt agggatcttc ttttaaatcc 300
accaccctat gagatttctt cagacattca agaggcatgc agacttatga tgagtgtcac 360
atgttcaatt cctgatttta cctgtatttc atctgcaaag ctgggtcaagc tgcttgagtt 420
gagggaggca aatcacgttg agttctgcaa aataaagagc atgggtcgaag agatactgca 480
gttgata 488

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<210> 38
<211> 3373
<212> DNA
<213> Lycopersicon esculentum

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<220>
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<222> (689)..(689)
<223> n is a, c, g, or t

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1231-218.ST25.txt

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cgagagcaga tacgttgcgt gaaggagcgg aagttttttg ccacaacggc aaaaaaactc 180
aaacaaccaa aaagtattcc agaggaaaaa gactatgtta atattatgtg gtggaaagag 240
agaatggaat tcttgagaaa gccttcttcc gctcttctgg ctaagaggct tacatattgt 300
aacttgctgg gtgtggatcc gagtttgaga aatggaagtc ttaaagaggg aacacttaac 360
tcggagatgt tgcagttcaa gtcaaaatth ccacgtgaag ttttgctctg tagagtaggt 420
gatttttatg aagctattgg attcgatgct tgtattcttg tggaatatgc tggtttaaatt 480
ccatttggtg gcctgcactc agatagtata ccaaagctg gttgtccagt tgtgaatcta 540
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1231-218.ST25.txt

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<210> 39
 <211> 3373
 <212> DNA
 <213> Lycopersicon esculentum

<220>
 <221> CDS
 <222> (1)..(3372)

1231-218.ST25.txt

<220>

<221> misc_feature

<222> (689)..(689)

<223> n is a, c, g, or t

<400> 39

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cgt	tca	ctg	tcc	ctt	ttc	ctc	cgt	cca	cca	ctt	cgc	cgg	cgt	ttc	tta	96
Arg	Ser	Leu	Ser	Leu	Phe	Leu	Arg	Pro	Pro	Leu	Arg	Arg	Arg	Phe	Leu	
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Ser	Phe	Ser	Pro	His	Thr	Leu	Cys	Arg	Glu	Gln	Ile	Arg	Cys	Val	Lys	
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gag	cgg	aag	ttt	ttt	gcc	aca	acg	gca	aaa	aaa	ctc	aaa	caa	cca	aaa	192
Glu	Arg	Lys	Phe	Phe	Ala	Thr	Thr	Ala	Lys	Lys	Leu	Lys	Gln	Pro	Lys	
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Ser	Ile	Pro	Glu	Glu	Lys	Asp	Tyr	Val	Asn	Ile	Met	Trp	Trp	Lys	Glu	
65					70					75					80	

aga	atg	gaa	ttc	ttg	aga	aag	cct	tct	tcc	gct	ctt	ctg	gct	aag	agg	288
Arg	Met	Glu	Phe	Leu	Arg	Lys	Pro	Ser	Ser	Ala	Leu	Leu	Ala	Lys	Arg	
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ctt	aca	tat	tgt	aac	ttg	ctg	ggt	gtg	gat	ccg	agt	ttg	aga	aat	gga	336
Leu	Thr	Tyr	Cys	Asn	Leu	Leu	Gly	Val	Asp	Pro	Ser	Leu	Arg	Asn	Gly	
			100				105						110			

agt	ctt	aaa	gag	gga	aca	ctt	aac	tcg	gag	atg	ttg	cag	ttc	aag	tca	384
Ser	Leu	Lys	Glu	Gly	Thr	Leu	Asn	Ser	Glu	Met	Leu	Gln	Phe	Lys	Ser	
		115					120					125				

aaa	ttt	cca	cgt	gaa	gtt	ttg	ctc	tgt	aga	gta	ggt	gat	ttt	tat	gaa	432
Lys	Phe	Pro	Arg	Glu	Val	Leu	Leu	Cys	Arg	Val	Gly	Asp	Phe	Tyr	Glu	
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Ala	Ile	Gly	Phe	Asp	Ala	Cys	Ile	Leu	Val	Glu	Tyr	Ala	Gly	Leu	Asn	
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cca	ttt	ggt	ggc	ctg	cac	tca	gat	agt	ata	cca	aaa	gct	ggt	tgt	cca	528
Pro	Phe	Gly	Gly	Leu	His	Ser	Asp	Ser	Ile	Pro	Lys	Ala	Gly	Cys	Pro	
				165					170					175		

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Val	Val	Asn	Leu	Arg	Gln	Thr	Leu	Asp	Asp	Leu	Thr	Arg	Asn	Gly	Phe	
			180					185					190			

tct	gtg	tgc	gtc	gtg	gag	gaa	gtt	cag	ggt	cca	act	caa	gct	cgt	gct	624
Ser	Val	Cys	Val	Val	Glu	Glu	Val	Gln	Gly	Pro	Thr	Gln	Ala	Arg	Ala	
		195					200					205				

cgt	aag	agt	cga	ttt	ata	tca	ggg	cat	gca	cat	cca	ggc	agt	ccc	tat	672
Arg	Lys	Ser	Arg	Phe	Ile	Ser	Gly	His	Ala	His	Pro	Gly	Ser	Pro	Tyr	
	210					215					220					

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1231-218.ST25.txt

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tct Ser	gtt Val	tac Tyr	gag Glu 260	act Thr	atg Met	aag Lys	act Thr	tac Tyr 265	tct Ser	gtg Val	gaa Glu	gat Asp	ggc Gly 270	cta Leu	act Thr	816
gaa Glu	gaa Glu	gcc Ala 275	gta Val	gtc Val	acc Thr	aaa Lys	ctt Leu 280	cgt Arg	act Thr	tgt Cys	cga Arg	tgc Cys 285	cat His	cat His	ttt Phe	864
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cag Gln	cag Gln	gaa Glu	tgg Trp	ttg Leu 325	gat Asp	ggc Gly	aat Asn	cct Pro	atc Ile 330	gat Asp	gag Glu	ctt Leu	ttg Leu	ttc Phe 335	aag Lys	1008
gta Val	aaa Lys	gag Glu	ctt Leu 340	tat Tyr	ggt Gly	ctc Leu	aat Asn	gat Asp 345	gac Asp	att Ile	cca Pro	ttc Phe	aga Arg 350	aat Asn	gtc Val	1056
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aca Thr	caa Gln 370	att Ile	ggt Gly	gct Ala	att Ile	cca Pro 375	acc Thr	gaa Glu	ggg Gly	att Ile	cca Pro 380	tgt Cys	ttg Leu	tta Leu	aag Lys	1152
gtg Val 385	ttg Leu	ctt Leu	cct Pro	cct Pro	cat His 390	tgc Cys	agt Ser	ggt Gly	cta Leu	cca Pro 395	gtc Val	ctg Leu	tat Tyr	att Ile	agg Arg 400	1200
gat Asp	ctt Leu	ctt Leu	tta Leu	aat Asn 405	cca Pro	cca Pro	gcc Ala	tat Tyr	gag Glu 410	att Ile	tct Ser	tca Ser	gac Asp	ata Ile 415	caa Gln	1248
gag Glu	gca Ala	tgc Cys	aga Arg 420	ctt Leu	atg Met	atg Met	agt Ser	gtc Val 425	aca Thr	tgt Cys	tca Ser	att Ile	cct Pro 430	gat Asp	ttt Phe	1296
acc Thr	tgt Cys	att Ile 435	tca Ser	tct Ser	gca Ala	aag Lys	ctg Leu 440	gtc Val	aag Lys	ctg Leu	ctt Leu	gag Glu 445	ttg Leu	agg Arg	gag Glu	1344
gca Ala	aat Asn 450	cac His	gtt Val	gag Glu	ttc Phe	tgc Cys 455	aaa Lys	ata Ile	aag Lys	agc Ser	atg Met 460	gtc Val	gaa Glu	gag Glu	ata Ile	1392
ctg Leu 465	cag Gln	ttg Leu	tat Tyr	aga Arg	aat Asn 470	tca Ser	gag Glu	ctt Leu	cgt Arg	gct Ala 475	atw Xaa	gta Val	gag Glu	tta Leu	ctg Leu 480	1440

1231-218.ST25.txt

atg gat cct act tgg gtg gca act ggg ttg aaa gtt gat ttt gat aca Met Asp Pro Thr Trp Val Ala Thr Gly Leu Lys Val Asp Phe Asp Thr 485 490 495	1488
cta gta aat gaa tgt gga aag att tct tgt aga atc agt gaa ata ata Leu Val Asn Glu Cys Gly Lys Ile Ser Cys Arg Ile Ser Glu Ile Ile 500 505 510	1536
tcc gta cat ggt gaa aat gat caa aag att agt tcc tat cct atc atc Ser Val His Gly Glu Asn Asp Gln Lys Ile Ser Ser Tyr Pro Ile Ile 515 520 525	1584
cca aat gat ttc ttt gaa gat atg gag ttg ttg tgg aaa ggc cgt gtc Pro Asn Asp Phe Phe Glu Asp Met Glu Leu Leu Trp Lys Gly Arg Val 530 535 540	1632
aag agg atc cat ttg gag gaa gca tat gca gaa gta gaa aag gct gcg Lys Arg Ile His Leu Glu Glu Ala Tyr Ala Glu Val Glu Lys Ala Ala 545 550 555 560	1680
gat gct tta tct tta gcc ata aca gaa gat ttc cta cct att att tca Asp Ala Leu Ser Leu Ala Ile Thr Glu Asp Phe Leu Pro Ile Ile Ser 565 570 575	1728
aga ata agg gcc acg atg gcc cca ctt gga gga act aaa ggg gag att Arg Ile Arg Ala Thr Met Ala Pro Leu Gly Gly Thr Lys Gly Glu Ile 580 585 590	1776
ttg tat gcc cgt gag cat gga gct gta tgg ttt aag gga aag aga ttt Leu Tyr Ala Arg Glu His Gly Ala Val Trp Phe Lys Gly Lys Arg Phe 595 600 605	1824
gta cca act gtt tgg gct gga acc gct gga gaa gaa caa att aag caa Val Pro Thr Val Trp Ala Gly Thr Ala Gly Glu Glu Gln Ile Lys Gln 610 615 620	1872
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aga aat tgg att ttc cca aca atc aca caa ttt aac aaa tgt cag gac Arg Asn Trp Ile Phe Pro Thr Ile Thr Gln Phe Asn Lys Cys Gln Asp 705 710 715 720	2160
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1231-218.ST25.txt

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gat atg cag tcc atg ttt ctt tta aca ggt cca aat ggt ggg ggc aaa Asp Met Gln Ser Met Phe Leu Leu Thr Gly Pro Asn Gly Gly Gly Lys 755 760 765	2304
tca agc ttg ctg cgt tcg ttg tgt gca gct gca ttg cta gga atg tgt Ser Ser Leu Leu Arg Ser Leu Cys Ala Ala Ala Leu Leu Gly Met Cys 770 775 780	2352
ggg ttc atg gtt cca gct gaa tca gct gtc att cct cat ttt gac tca Gly Phe Met Val Pro Ala Glu Ser Ala Val Ile Pro His Phe Asp Ser 785 790 795 800	2400
att atg ctg cat atg aaa tca tat gat agt cct gtt gat gga aaa agt Ile Met Leu His Met Lys Ser Tyr Asp Ser Pro Val Asp Gly Lys Ser 805 810 815	2448
tca ttt cag att gaa atg tct gaa att cgg tct ctg att act ggt gcc Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Ile Thr Gly Ala 820 825 830	2496
act tca aga agt ctt gta ctt ata gat gaa ata tgt cga gga aca gaa Thr Ser Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg Gly Thr Glu 835 840 845	2544
aca gca aaa ggg aca tgt att gct gga agt gtc ata gaa acc ctg gac Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Val Ile Glu Thr Leu Asp 850 855 860	2592
gaa att ggc tgt ttg gga att gta tca acc cac ttg cat gga ata ttt Glu Ile Gly Cys Leu Gly Ile Val Ser Thr His Leu His Gly Ile Phe 865 870 875 880	2640
gat tta ccc ctg aaa atc aag aag acc gtg tat aaa gca atg gga gct Asp Leu Pro Leu Lys Ile Lys Lys Thr Val Tyr Lys Ala Met Gly Ala 885 890 895	2688
gaa tat gtt gac ggt caa cca ata cca act tgg aaa ctc att gat ggg Glu Tyr Val Asp Gly Gln Pro Ile Pro Thr Trp Lys Leu Ile Asp Gly 900 905 910	2736
atc tgt aaa gag agt cta gca ttt gaa aca gct cag aga gaa gga att Ile Cys Lys Glu Ser Leu Ala Phe Glu Thr Ala Gln Arg Glu Gly Ile 915 920 925	2784
cca gaa ata tta atc caa aga gca gaa gaa ttg tat aat tca gct tac Pro Glu Ile Leu Ile Gln Arg Ala Glu Glu Leu Tyr Asn Ser Ala Tyr 930 935 940	2832
ggg aat cag ata cca agg aag ata gac caa ata aga cct ctt cgt tca Gly Asn Gln Ile Pro Arg Lys Ile Asp Gln Ile Arg Pro Leu Arg Ser 945 950 955 960	2880
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1231-218.ST25.txt

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		995					1000					1005								
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Lys	Lys	Leu	Ile	Glu	Leu	Tyr	Lys	Met	Lys	Asn	Pro	Ser	Glu	Met						
	1010					1015					1020									
cca	atg	gtg	aat	tgc	gtt	ctt	att	gct	gcc	agg	gaa	cag	ccg	gct		3114				
Pro	Met	Val	Asn	Cys	Val	Leu	Ile	Ala	Ala	Arg	Glu	Gln	Pro	Ala						
	1025					1030					1035									
cca	tca	aca	att	ggt	gct	tca	agt	gtc	tat	ata	atg	cta	aga	cct		3159				
Pro	Ser	Thr	Ile	Gly	Ala	Ser	Ser	Val	Tyr	Ile	Met	Leu	Arg	Pro						
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Asp	Lys	Lys	Leu	Tyr	Val	Gly	Gln	Thr	Asp	Asp	Leu	Glu	Gly	Arg						
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Val	Arg	Ala	His	Arg	Leu	Lys	Glu	Gly	Met	Glu	Asn	Ala	Ser	Phe						
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cta	tat	ttc	tta	gtc	tct	ggc	aag	agc	atc	gcc	tgc	caa	ttg	gaa		3294				
Leu	Tyr	Phe	Leu	Val	Ser	Gly	Lys	Ser	Ile	Ala	Cys	Gln	Leu	Glu						
	1085					1090					1095									
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Thr	Leu	Leu	Ile	Asn	Gln	Leu	Pro	Asn	His	Gly	Phe	Gln	Leu	Thr						
	1100					1105					1110									
aac	gtt	gct	gat	ggt	aag	cat	cgt	aat	ttt	ggc	a					3373				
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 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <221> misc_feature
 <222> (230)..(230)
 <223> The 'Xaa' at location 230 stands for Glu, Gly, Ala, or Val.

<220>
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 <222> (476)..(476)
 <223> The 'Xaa' at location 476 stands for Ile.

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Arg	Ser	Leu	Ser	Leu	Phe	Leu	Arg	Pro	Pro	Leu	Arg	Arg	Arg	Phe	Leu
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1231-218.ST25.txt

Ser Phe Ser Pro His Thr Leu Cys Arg Glu Gln Ile Arg Cys Val Lys
 35 40 45
 Glu Arg Lys Phe Phe Ala Thr Thr Ala Lys Lys Leu Lys Gln Pro Lys
 50 55 60
 Ser Ile Pro Glu Glu Lys Asp Tyr Val Asn Ile Met Trp Trp Lys Glu
 65 70 75 80
 Arg Met Glu Phe Leu Arg Lys Pro Ser Ser Ala Leu Leu Ala Lys Arg
 85 90 95
 Leu Thr Tyr Cys Asn Leu Leu Gly Val Asp Pro Ser Leu Arg Asn Gly
 100 105 110
 Ser Leu Lys Glu Gly Thr Leu Asn Ser Glu Met Leu Gln Phe Lys Ser
 115 120 125
 Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val Gly Asp Phe Tyr Glu
 130 135 140
 Ala Ile Gly Phe Asp Ala Cys Ile Leu Val Glu Tyr Ala Gly Leu Asn
 145 150 155 160
 Pro Phe Gly Gly Leu His Ser Asp Ser Ile Pro Lys Ala Gly Cys Pro
 165 170 175
 Val Val Asn Leu Arg Gln Thr Leu Asp Asp Leu Thr Arg Asn Gly Phe
 180 185 190
 Ser Val Cys Val Val Glu Glu Val Gln Gly Pro Thr Gln Ala Arg Ala
 195 200 205
 Arg Lys Ser Arg Phe Ile Ser Gly His Ala His Pro Gly Ser Pro Tyr
 210 215 220
 Val Phe Gly Leu Val Xaa Asp Asp Gln Asp Leu Asp Phe Pro Glu Pro
 225 230 235 240
 Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys Gly Tyr Cys Ile Ile
 245 250 255
 Ser Val Tyr Glu Thr Met Lys Thr Tyr Ser Val Glu Asp Gly Leu Thr
 260 265 270
 Glu Glu Ala Val Val Thr Lys Leu Arg Thr Cys Arg Cys His His Phe
 275 280 285

1231-218.ST25.txt

Phe Leu His Asn Ser Leu Lys Asn Asn Ser Ser Gly Thr Ser Arg Trp
 290 295 300

Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly Glu Cys Asn Ala Arg
 305 310 315 320

Gln Gln Glu Trp Leu Asp Gly Asn Pro Ile Asp Glu Leu Leu Phe Lys
 325 330 335

Val Lys Glu Leu Tyr Gly Leu Asn Asp Asp Ile Pro Phe Arg Asn Val
 340 345 350

Thr Val Val Ser Glu Asn Arg Pro Arg Pro Leu His Leu Gly Thr Ala
 355 360 365

Thr Gln Ile Gly Ala Ile Pro Thr Glu Gly Ile Pro Cys Leu Leu Lys
 370 375 380

Val Leu Leu Pro Pro His Cys Ser Gly Leu Pro Val Leu Tyr Ile Arg
 385 390 395 400

Asp Leu Leu Leu Asn Pro Pro Ala Tyr Glu Ile Ser Ser Asp Ile Gln
 405 410 415

Glu Ala Cys Arg Leu Met Met Ser Val Thr Cys Ser Ile Pro Asp Phe
 420 425 430

Thr Cys Ile Ser Ser Ala Lys Leu Val Lys Leu Leu Glu Leu Arg Glu
 435 440 445

Ala Asn His Val Glu Phe Cys Lys Ile Lys Ser Met Val Glu Glu Ile
 450 455 460

Leu Gln Leu Tyr Arg Asn Ser Glu Leu Arg Ala Xaa Val Glu Leu Leu
 465 470 475 480

Met Asp Pro Thr Trp Val Ala Thr Gly Leu Lys Val Asp Phe Asp Thr
 485 490 495

Leu Val Asn Glu Cys Gly Lys Ile Ser Cys Arg Ile Ser Glu Ile Ile
 500 505 510

Ser Val His Gly Glu Asn Asp Gln Lys Ile Ser Ser Tyr Pro Ile Ile
 515 520 525

Pro Asn Asp Phe Phe Glu Asp Met Glu Leu Leu Trp Lys Gly Arg Val
 Page 101

530

535

Lys Arg Ile His Leu Glu Glu Ala Tyr Ala Glu Val Glu Lys Ala Ala
545 550 555 560

Asp Ala Leu Ser Leu Ala Ile Thr Glu Asp Phe Leu Pro Ile Ile Ser
565 570 575

Arg Ile Arg Ala Thr Met Ala Pro Leu Gly Gly Thr Lys Gly Glu Ile
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Leu Tyr Ala Arg Glu His Gly Ala Val Trp Phe Lys Gly Lys Arg Phe
595 600 605

Val Pro Thr Val Trp Ala Gly Thr Ala Gly Glu Glu Gln Ile Lys Gln
610 615 620

Leu Arg Pro Ala Leu Asp Ser Lys Gly Lys Lys Val Gly Glu Glu Trp
625 630 635 640

Phe Thr Thr Met Arg Val Glu Asp Ala Ile Ala Arg Tyr His Glu Ala
645 650 655

Ser Ala Arg Ala Lys Ser Arg Val Leu Glu Leu Leu Arg Gly Leu Ser
660 665 670

Ser Glu Leu Leu Ser Lys Ile Asn Ile Leu Ile Phe Ala Ser Val Leu
675 680 685

Asn Val Ile Ala Lys Ser Leu Phe Ser His Val Ser Glu Gly Arg Arg
690 695 700

Arg Asn Trp Ile Phe Pro Thr Ile Thr Gln Phe Asn Lys Cys Gln Asp
705 710 715 720

Thr Glu Ala Leu Asn Gly Thr Asp Gly Met Lys Ile Ile Gly Leu Ser
725 730 735

Pro Tyr Trp Phe Asp Ala Ala Arg Gly Thr Gly Val Gln Asp Thr Val
740 745 750

Asp Met Gln Ser Met Phe Leu Leu Thr Gly Pro Asn Gly Gly Gly Lys
755 760 765

Ser Ser Leu Leu Arg Ser Leu Cys Ala Ala Ala Leu Leu Gly Met Cys
770 775 780

Gly Phe Met Val Pro Ala Glu Ser Ala Val Ile Pro His Phe Asp Ser
 785 790 795 800

Ile Met Leu His Met Lys Ser Tyr Asp Ser Pro Val Asp Gly Lys Ser
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Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Ile Thr Gly Ala
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Thr Ser Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg Gly Thr Glu
 835 840 845

Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Val Ile Glu Thr Leu Asp
 850 855 860

Glu Ile Gly Cys Leu Gly Ile Val Ser Thr His Leu His Gly Ile Phe
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Asp Leu Pro Leu Lys Ile Lys Lys Thr Val Tyr Lys Ala Met Gly Ala
 885 890 895

Glu Tyr Val Asp Gly Gln Pro Ile Pro Thr Trp Lys Leu Ile Asp Gly
 900 905 910

Ile Cys Lys Glu Ser Leu Ala Phe Glu Thr Ala Gln Arg Glu Gly Ile
 915 920 925

Pro Glu Ile Leu Ile Gln Arg Ala Glu Glu Leu Tyr Asn Ser Ala Tyr
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Gly Asn Gln Ile Pro Arg Lys Ile Asp Gln Ile Arg Pro Leu Arg Ser
 945 950 955 960

Asp Ile Asp Leu Asn Ser Thr Asp Asn Ser Ser Asp Gln Leu Asn Gly
 965 970 975

Thr Arg Gln Ile Ala Leu Asp Ser Ser Thr Lys Leu Met His Arg Met
 980 985 990

Gly Ile Ser Ser Lys Lys Leu Glu Asp Ala Ile Cys Leu Ile Cys Glu
 995 1000 1005

Lys Lys Leu Ile Glu Leu Tyr Lys Met Lys Asn Pro Ser Glu Met
 1010 1015 1020

Pro Met Val Asn Cys Val Leu Ile Ala Ala Arg Glu Gln Pro Ala
 1025 1030 1035

1231-218.ST25.txt

Pro Ser Thr Ile Gly Ala Ser Ser Val Tyr Ile Met Leu Arg Pro
1040 1045 1050

Asp Lys Lys Leu Tyr Val Gly Gln Thr Asp Asp Leu Glu Gly Arg
1055 1060 1065

Val Arg Ala His Arg Leu Lys Glu Gly Met Glu Asn Ala Ser Phe
1070 1075 1080

Leu Tyr Phe Leu Val Ser Gly Lys Ser Ile Ala Cys Gln Leu Glu
1085 1090 1095

Thr Leu Leu Ile Asn Gln Leu Pro Asn His Gly Phe Gln Leu Thr
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1115 1120

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<213> Triticum aestivum

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<212> PRT
<213> Triticum aestivum

<400> 42

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1231-218.ST25.txt

Thr Ile Cys Lys Asp Lys Leu Leu Asp Leu Tyr Asn Lys Arg Ser Ile
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Ser Glu Leu Val Glu Val Val Cys Val Thr Val Gly Ala Arg Glu Gln
35 40 45

Pro Pro Pro Ser Thr Val Gly Arg Ser Ser Ile Tyr Ile Ile Ile Arg
50 55 60

Arg Asp Asn Lys Leu Tyr Val Gly Gln Thr Asp Asp Leu Val Gly Arg
65 70 75 80

Leu Gly Ala His Arg Ser Lys Glu Gly Met Gln Asp Ala Thr Ile Leu
85 90 95

Tyr Ile Ile Val Pro Gly Lys Ser Val Ala Cys Gln Leu Glu Thr Leu
100 105 110

Leu Ile Asn Gln Leu Pro Thr Lys Gly Phe Lys Leu Thr Asn Lys Ala
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Met Ala Ala His
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<213> Zinnia elegans

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1231-218.ST25.txt

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Leu Gly Gly Pro Lys Gly Glu Ile Leu Tyr Val Arg Glu His Lys Ala
 50 55 60

Ile Trp Phe Lys Gly Lys Arg Phe Val Pro Thr Ile Gly Ala Asn Thr
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Pro Val Glu Lys Gln Ile Lys Gln Leu Lys Pro Ser Val Asp Ser Lys
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Gly Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Ser Lys Val Glu Asp
 100 105 110

Ala Leu Ser Arg Tyr His Glu Ala Gly Ala Lys Ala Lys Ser Met Val
 115 120 125

Leu Glu Leu Leu Arg Gly Leu Ser Ala Glu Leu Gln Ala Glu Ile Asn
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 <213> Phaseolus vulgaris

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ataaatggac gtgtcaagaa tgtatcaact tatatggata ataacagggg ttcaagggga 180

1231-218.ST25.txt

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1231-218.ST25.txt

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1231-218.ST25.txt																
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Trp	Glu	Met	Leu	Gln	Phe	Lys	Ser	Lys	Phe	Pro	Arg	Gln	Val	Leu	Leu	
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1231-218.ST25.txt

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cga Arg	cct Pro 370	tta Leu	acc Thr	ctt Leu	gga Gly	aca Thr 375	tct Ser	act Thr	caa Gln	att Ile	ggg Gly 380	gcc Ala	att Ile	cat His	acg Thr	1152
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1231-218.ST25.txt

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gag Glu	tct Ser	aaa Lys	tgg Trp	aaa Lys	ggg Gly	cga Arg	ata Ile	aaa Lys	aga Arg	gtc Val	cat His	ata Ile	gat Asp	gag Glu	gtg Val	1680
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1231-218.ST25.txt

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aga Arg	tcc Ser	atc Ile 835	att Ile	ggc Gly	gga Gly	acc Thr	acc Thr 840	aaa Lys	agg Arg	agc Ser	ctt Leu	gta Val 845	ctt Leu	gtt Val	gat Asp	2544
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1231-218.ST25.txt

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<400> 47

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Thr Lys Lys Pro Lys Val Pro Asn Asn Val Leu Asp Asp Lys Asp Leu
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85 90 95

Ser Thr Val Gln Leu Ile Gln Arg Leu Glu Phe Ser Asn Leu Leu Gly
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Leu Asp Ser Lys Leu Lys Asn Gly Ser Val Lys Glu Gly Thr Leu Asn
Page 113

115

120

125

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 Cys Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Val
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 Gln Gly Pro Thr Gln Ala Arg Ser Arg Lys Arg Arg Phe Ile Ser Gly
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 260 265 270
 Tyr Ser Tyr Glu Asp Cys Leu Thr Glu Glu Ala Ile Val Thr Lys Leu
 275 280 285
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 305 310 315 320
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 325 330 335
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 355 360 365

1231-218.ST25.txt

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 515 520 525
 Lys Ile Asn Ser Leu Ser Ile Ile Pro Tyr Glu Phe Phe Glu Asp Thr
 530 535 540
 Glu Ser Lys Trp Lys Gly Arg Ile Lys Arg Val His Ile Asp Glu Val
 545 550 555 560
 Phe Thr Ala Val Gln Lys Ala Ala Glu Val Leu His Ile Ala Val Thr
 565 570 575
 Glu Asp Phe Val Pro Val Val Ser Arg Val Lys Ala Thr Ile Ala Pro
 580 585 590
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 595 600 605
 Val Trp Phe Arg Gly Lys Arg Phe Thr Pro Ser Leu Trp Ser Gly Ser
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1231-218.ST25.txt

Pro Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys
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660 665 670

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675 680 685

Ile Leu Val Phe Ser Ser Thr Leu Leu Val Ile Thr Lys Ala Leu Phe
690 695 700

Ala His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu
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Ala Glu Ser Asn Gly Phe Glu Asp Val Lys Ser Ser Asp Lys Ile His
725 730 735

Gly Met Lys Ile Val Gly Leu Ala Pro Tyr Trp Phe His Ile Ala Glu
740 745 750

Gly Ile Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr
755 760 765

Gly Pro Asn Gly Gly Gly Lys Ser Ser Leu Leu Arg Ser Ile Cys Ala
770 775 780

Ala Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala
785 790 795 800

Val Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp
805 810 815

Ser Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu
820 825 830

Arg Ser Ile Ile Gly Gly Thr Thr Lys Arg Ser Leu Val Leu Val Asp
835 840 845

Glu Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly
850 855 860

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865 870 875 880

1231-218.ST25.txt

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900 905 910

Thr Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu
915 920 925

Thr Ala Ile Arg Glu Gly Ile Pro Glu Pro Ile Ile Arg Arg Ala Glu
930 935 940

Cys Leu Tyr Lys Ser Val Tyr Ala Glu Glu Asn Phe Pro Asn Glu Glu
945 950 955 960

Lys Phe Ser Thr Cys Asn Asn Leu Asn Asn Leu Asn Thr Thr Ser Leu
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 Ala Lys Arg Glu Gly Ile Pro Glu Xaa Ile Ile Arg Arg Ala Glu
 1355 1360 1365
 Xaa Leu Tyr Xaa Ser Val Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1370 1375 1380
 Xaa Xaa Xaa Xaa Xaa Glu Lys Xaa Ser Xaa Xaa Ile Asn Ile Xaa
 1385 1390 1395
 Asn Leu Xaa Thr Thr Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1400 1405 1410

1231-218.ST25.txt

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Met	Xaa	Ile	Leu	Arg	Lys	Glu
	1415					1420					1425			
Leu	Glu	Arg	Ala	Ile	Thr	Val	Ile	Cys	Xaa	Lys	Lys	Ile	Ile	Glu
	1430					1435					1440			
Leu	Xaa	Xaa	Lys	Lys	Xaa	Xaa	Xaa	Glu	Leu	Xaa	Glu	Ile	Xaa	Cys
	1445					1450					1455			
Leu	Leu	Ile	Gly	Ala	Arg	Glu	Gln	Pro	Pro	Pro	Ser	Thr	Val	Gly
	1460					1465					1470			
Ser	Ser	Ser	Val	Tyr	Val	Met	Xaa	Arg	Pro	Asp	Lys	Lys	Leu	Tyr
	1475					1480					1485			
Val	Gly	Gln	Thr	Asp	Asp	Leu	Glu	Gly	Arg	Val	Arg	Ala	His	Arg
	1490					1495					1500			
Leu	Lys	Glu	Gly	Met	Xaa	Asp	Ala	Ser	Phe	Leu	Tyr	Phe	Leu	Val
	1505					1510					1515			
Pro	Gly	Lys	Ser	Ile	Ala	Cys	Gln	Leu	Glu	Thr	Leu	Leu	Ile	Asn
	1520					1525					1530			
Gln	Leu	Xaa	Xaa	Gln	Gly	Phe	Gln	Leu	Ser	Asn	Ile	Ala	Asp	Gly
	1535					1540					1545			
Lys	His	Arg	Asn	Phe	Gly	Thr	Ser	Xaa	Leu					
	1550					1555								